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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

### Result No. ი a Score Query Match 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 2116 165789 286098 6023 6210 135050 140335 16803 16803 174298 181848 181893 197795 202267 207930 2015 Length DB SYNINFOSP AX774881 AK097379 AX587848 AX014320 BD222199 HSM807248 196207 AX330284 AR272850 AR276423 AR276431 AR406706 AR406706 AX062944 AX062952 AX367861 AX367869 HUMFOS AC118536 AC118538 AC147196 AC120514 CNS07YOR AC119064 AC117934 AC117934 AX340922 AX587935 ü AX336394 AX340922 Sequence AX587935 Sequence AX587935 Sequence AX2888 Synthetic ( AX774881 Sequence AX074881 Sequence AX07479 Homo sapi AX587848 Sequence AX014320 Sequence AX014320 Sequence BX647104 Homo sapi 196207 Sequence AX336334 Sequence AX336338 Sequence AX336328 Sequence AX13210 Sus scrof AX212879 Homo sapi AX653628 Sequence AX063638 Felis cat AC147196 Sus scrof AC118536 Felis cat AC147196 Sus scrof AC117932 Papio anu AC117932 Papio anu AC117932 Papio anu AF111167 Homo sapi AC120203 Pan trogl AC120203 Pan trogl AC120203 Pan trogl AC120304 Sequence AX277842 Sequence AX277843 Sequence AX277843 Sequence AX367861 Sequence AX367869 Sequence AX367869 Sequence AX367869 Sequence AX367869 Sequence AX367869 Sequence AX367861 Sequence AX367863 Rattus no AC119054 Rattus no AC119054 Rattus no AC119054 Rattus no AC119135 Rattus no AC119155 Requence AX36787 Sequence Description

## ALIGNMENTS

TITLE C	EFERENCE 1	OURCE H	z ő	ESULT 1 .X340922/c
Jiang, Y., Harlocker, S.L. and Secrist, H. Compositions and methods for the therapy and diagnosis of colon cancer	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1	Homo sapiens (human)	Sequence 1169 from Patent WO0196388. AX340922 AX340922.1 GI:18136904	AX340922 242 bp DNA linear PAT 10-JAN-2002

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Synthetic (plasmid psoIF
mRNA, 3'UTR.
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synthetic construct
                                                       M28858
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Sequence 405 from Patent
AX587935
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llarity 100.0%;
Conservative 0
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viral oncogene homolog (FOS) gene."
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 197 from Patent
AX774881
AX774881.1 GI:32486397
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Kruys,V., Marinx,O., Shaw,G., Deschamps,J. and Huez,G.
Translational blockade imposed by cytokine-derived UA-rich
  AK097379
                                                                                                                                                           h 100.0%; Score 73; DB 6; L Similarity 100.0%; Pred. No. 0.00036; O: Mismatches 0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:32630"
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2 (bases 2 to 1918)
2 (bas
Pert, V.
Gene expression profiling of primary breast carcinomas using arrays
                                                                                                                                                                                                                                                                                                             Sequence 318 from Patent AX587848
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                                                                           Bertucci, F., Houlgatte, R.,
                                                                                                                                         artificial sequences.
                                                                                                                                                                           synthetic construct synthetic construct
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Location/Qualifiers
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Homo sapiens (human)
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/mol type="mRNA"
/db_ref="taxon:9606"
/clone="TCOLN2000236"
/tissue type="colon, tumor tissue"
/clone_Tib="TCOLN2"
/note="cloning vector: pME18SFL3"
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Pred. No. 0.00024;
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WO0246467
                                                                        Birnbaum, D.,
                                                                        Nguyen, C., Viens, P.
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Human nucleic acid sequence originating in 
BD222199
BD222199.1 GI:33031969
JP 2002512017-A/28.
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Sequence 28 from Patent WO9954353.
AX014320
AX014320.1 GI:10040674
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                                                      BD222199
                                                                                                                                                                                                                                                                                                                                                                      Human nucleic acid sequences of normal uterus tissue Patent: WO 9954353-A 28 28-OCT-1999; SCHMITT ARMIN (DB); SPECHT THOMAS (DE); DAHL EDGAR (IBERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GJ (DE); PILARSKY CHRISTIAN (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. Pilarsky,C.
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Mammalia; Eutheria; Primates;
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Patent: WO 0246467-A 318 13-JUN-2002;
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homolog (FOS) gene."
                                                                                                                                                                                                                                                                                                    mol_type="unassigned"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Pred. No. 0.00023;
Mismatches 0;
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Pred. No. 0.00023;
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                        Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s. Wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZ)6860904124) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 2121)
Wambutt, R., Heubner, D., Mewes, H.W.,
Fobo, G., Han, M. and Wiemann, S.
The German Human cDNA Consortium
                                                                                                                                                                                                                               Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Specht, T., Hinzmann, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSM807248
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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17-APR-1998 DE 198 17 946.4
THOWAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
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BIN GESELLSCHAFT FUER GENOM FORSCHUNG
HOMO SADIENS (human)
JP 2002512017-A/28
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0.00023;
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 3565)
Calabretta, B. and Skorski, T.
Antisense oligonucleotides targeting
Patent: US 5734039-A 44 31-MAR-1998;
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/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                          /organism="unknown"
/mol_type="unassigned
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                           GI:18103262
  Chordata;
Primates;
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                                                                                                                                                                                                                                                Score 73; DB b; L
Pred. No. 0.0002;
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Pred. No. 0.00023;
; Mismatches 0;
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  Craniata; Vertebrata; Catarrhini; Hominidae;
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RESULT 13
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Sequence 6903 from Patent WO0194629.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (human)
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Cancer gene determination and therapeutic screening using signature
                                                                           AX663638
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 0194629-A 6903 13-DEC-2001; Avalon Pharmaceuticals (US)
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Similarity 100.0%; F
73; Conservative 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                            GI:29163846
                                                           from Patent
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Pred. No. 0.0002;
); Mismatches 0
                                                           3565 bp
W002097127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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                                                                         PAT 22-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 09-JAN-2002
                                                                                                                                                                                                                                                                           0,
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                                                                                                            mRNA
                                                                                                                                                      precursor_RNA
                                                                                                                                                                                                                                  precursor_RNA
                                                                                                                                                                                         mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                         Complete nucleotide sequence of a human c-onc gene: deduced acid sequence of the human c-fos protein Proc. Natl. Acad. Sci. U.S.A: 80 (11), 3183-3187 (1983)
                                                                                                                                                                                                                                                                                                                                              Data kindly reviewed (10-OCT-1983)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3565)

van Straaten, F., Muller, R., Curran, T., Van Beveren, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and treatment of chronic lung disease
Patent: WO 02097127-A 13 05-DEC-2002;
Bayer Akthengesellschaft (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oellers, N., Gehrmann, M., Kallabis, H., Hall, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verma, I.M.
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                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
132. .3515
                                                                                                                                                      /note="possible transcript"
join(132. .429,1183. .1434,1866. .1973,2088.
/gene="c-fos"
132. .>3259
                                                                                                                                                                                                                                   132. .>3515
                                                                                                          /note="possible transcript"
join(132. .429,1183. .1434,1866.
gene="c-fos"
                             number=1
                                                           gene="c-fos"
                                                                             .32. .429
                                                                                          gene="c-fos"
                                                                                                                                        gene="c-fos"
                                                                                                                                                                                                                   'gene="c-fos"
                                                                                                                                                                                                                                                  gene="c-fos"
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/mol_type="unassigned DNA"
                                          note="(alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned
/db_xref="taxon:9606"
              .>3515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 73; DB 6;
100.0%; Pred. No. 0.0002;
tive 0; Mismatches (
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                                                                                                            .1973,2088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis, prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 21-NOV-1994
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  SSC132510
Sus scrofa c-fos gene, e
AJ132510
AJ132510.1 GI:4581530
c-fos gene.
Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                      61
                                                                                                                                                                                                                                                ch 100.0%;
l Similarity 100.0%;
73; Conservative 0;
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SSRPSGSETARSVPDMDLSGSFYAADWEPLHSGSLGMGPMATELEPLCTPVVTCTPSC
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                                                                                                                                                                                                                                                                                                                               note="(alternate
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Naqdfctdlavssanfiptutaistspdlqmlydpalyssvassgtraphpfgvpaps
Agaysragyvktmtggragsigrrgkveglspeeeekkritrernkmaaakcknkrrb
Ltdtlqaetdqledeksalqteianllkekeklefilaahrpackipddlgfpeemsv
                                                                                                                                                                                                                                                                                                                                           gene="c-fos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/proteIn_id="CAA24756.1"
/db_xref="GI:29904"
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136. .>3259
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|oin(136. .429,1183. .1434,1866.
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gene="c-fos"
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.36. .429
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866. .1973
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                                                                                                                                                                                                                                                                                                                                                                                                                      note="intron III"
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3905 AACGTTTATTGTGTTTTTAATTTATTTAATGATGGATTCTCAGATATTTATATTTTT
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                                                      h 100.0%;
Similarity 100.0%;
73; Conservative 0
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                     AACGTTTTATTGTGTTTTTAATTTTATTTATAGATGGATTCTCAGATATTTATATTTTT
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                                                                                                                               2639. .3280
/gene="c-fos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="c-Fos protein"
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/db_xref="GI:4581531"
                                                                                                                                                                                                                                                                1968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(817. .957,1716. .1967,2408.
/gene="c-fos"
join(817. .957,1716. .1967,2408.
/gene="c-fos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="GOA:097930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="c-fos"
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                                                                                                                      'number=4
                                                                                                                                                       number=3
                                                                                                                                                                                                          gene="c-fos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1/
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                                                                                                                                                                      gene="c-fos"
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                                                                                                                                                                                                                                                 gene="c-fos"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _rref="genomic DNA"
_xref="taxon:9823"
                                                                                                                                                                                                                                                           .2407
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                                                       0
                                                                  Score 73; DB 4;
Pred. No. 0.00019;
                                                        Mismatches
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Reiner,G., Heinricy,L., Brenig,B., Geldermann,H. and Dzapo,V. Cloning, structural organization, and chromosomal assignment of the porcine c-fos proto-oncogene, FOS Cytogenet. Cell Genet. 89 (1-2), 59-61 (2000) 20354993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-JAN-1999) Heinricy J.L., Anim Genetics, Justus-Liebig-University Giessen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASLDLSGGLPEAATPESEEAFTLPLLNDPEPKPSVEPVKNVSSMELKAEPFDDFLFPA
SSRPGGSETARSVPDMDLSGSFYAADWEPLHGGSLGMGPMATELEPLCTPVVTCTPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="Sptrembl:097930"
/translation="MMFSGFWADYEASSRCSSASPAGDSLSYYHSPADSFSSMGSPV
/translation="MMFSGFWADYEASSRCSSASPAGDSLSYYHSPADSFSSMGSPV
NAQDFCTDLAVSSANFIPTUTAISTSPDLQWLVQPTLVSSVAPSQTRAPHPYGVPTPS
AGAYSRAGTVXTMPGGRAQSIGRRGKVEQLSPEEEKKRIRRERE
LTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFILAAHRPACKIPDDLGFPEEMSV
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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               AAD46901
ABL97414
ACH22964
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ABZ3131
ADE84973
ADD29870
AAJ135207
AAJ134869
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AAK03464
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AAK03461
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ABV4337
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ABV4337
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       Aai03394
Abs03451
Abv94327
Aaz41352
Adb47308
Ach04087
Abq54467
                                                               Abx62923
Add29870
Aai13509
Aba55207
Aai34869
Aba44752
Aba24954
Aak28922
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Abz35131
                                                                                                                                                     Aad46901 C-fos 3'
Abl37580 Human co
                                                                                                                          Ade84978
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Human col
Breast ca
Human adu
Human gen
Farnesyl
Human tum
Probe #35
Human bra
Human bra
Human bra
Probe #34
Human bra
Human bra
Probe #35
Human col
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73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	ļ
100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	•	100.0	٠	
16595	16595	16595	6210	6210	6210	6210	6210	6210	6210	3565	3565	3565	3565	3565	3565	3565	3568	3565	3514	2461	2461	
7		ω																				
ABZ96789	AAF21095	AAA34973	ABZ96785	ACC46752	ABZ35089	ABT10875	AAF21091	AAA34969	AAQ63815	ABZ96786	ACC46762	ABK64754	ABK84488	ABL62456	ABL68566	AAF21092	AAA34970	AAV20466	ABK50444	AAH33223	AAC98119	
Abz96789	Aaf21095	Aaa34973	Abz96785	Acc46752	Abz35089	Abt10875	- Aaf21091	Aaa34969	Aaq63815	Abz96786	Acc46762	Abk64754	Abk84488	Ab162456	Ab168566	Aaf21092	Aaa34970	Aav20466	Abk50444	Aah33223	Aac98119	
Human	Human	c-fos	Human	Human	Human	Human	Colon	Kidney	Human	Human	Human	Human	Human	Human								
nuc	low	ade	nuc	မ္မ	gen	bre	low	ade	gen	nuc	පි	ben	CDN		Ca	low	ade	c-f	۷-£	co1	CO.	

# RESULT 1 AAD46901 AAD46901 standard; DNA; 75 ВP

ALIGNMENTS

C-fos 3' UTR ARE 27-JAN-2003 AAD46901; (first DNA entry)

Gene expression; transcript stability; drug screening; AU-rich element; ARB; c-fos; ds.

Mammalia.

WO200272844-A1.

19-SEP-2002.

08-MAR-2002; 2002WO-AU000351

09-MAR-2001; 2001US-0274770P

(GENE-) GENE STREAM PTY LTD.

Daly J;

WPI; 2002-759847/82.

New expression vector useful for modulating gene expression, identifying and analyzing regulatory sequences, new targets and reagents for treating human diseases, comprises a transcribable polynucleotide encoding an RNA element.

Claim 11; Page 59; 103pp; English

The present invention relates to novel expression vectors and/or reporter vectors providing kinetics of protein expression with improved temporal correlation to the promoter activity. The expression vectors comprise transcribable polynuclectides having sequences of nucleotides encoding RNA elements which modulates the stability of a transcript corresponding to the transcribable polynucleotide. The expression vectors are useful for modulating the stability of a transcript and determining expression of a polynucleotide of interest. They are useful for modulating gene expression, identifying and analysing regulatory sequences, new targets and reagents for treating human diseases and for drug screening. The

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RESULT 2
ABL37580/c
ID ABL375
XX ABL375
XX ABL375
XX OB-APR
XX Human;
XW Human;
XW Colon
XX Homo 8
XX WO2001
XX WO2001
XX OB-JUN
PR 20-DEC
XX OB-JUN
PR 20-FEB
XX UPI; 2
PT Novel
PT Useful
XX VIang
XX Claim
XX CC ABL364
CC Which
CC Produc
CC Specif
CC Used a
                                                                             Query Match
Best Local 9
                                                             Matches
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                                                                                                                                                        ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of canoer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114514/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUN-2000; 2000US-0210899P.
20-FEB-2001; 2001US-0270216P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon tumour antigen; cytostatic; vaccine; colon tumour metastatic antigen; diagnosis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is c\text{-fos}\ 3' UTR ARE (AU-rich element) DNA. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon tumour antigen polynucleotide SEQ ID NO:1169
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                                                                                                                                                                                                                                                                                                                                                          isolated colon tumor polynucleotide differentially expressed in tumor or colon metastatic tumor and polypeptides encoded by their for inhibiting development of cancer in patient.
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                                                                              Similarity
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                                                                                                                             242
                  AACGTTTTATTGTGTTTTTAATTTTATTTAAGATGGATTCTCAGATATTTTATATTTTT
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1169; 105pp; English.
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AACGITTTATTGTGTTTTTAATTTATTTAAGATGGATTCTCAGATATTTATATTTTT
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                                                           100.0%;
llarity 100.0%;
Conservative
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                                                                                                                           BP;
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                                                                                                                             102
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Pred. No. 7.1
0; Mismatches
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                                                                             Score 73;
Pred. No.
                                                             Mismatches
                                                                                                                           78
                                                                                                                           T; 0 U; 3 Other;
                                                                         6.2e-06;
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                                                                                            DB 6;
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                                                             Gaps
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밁 8

190

131

Query Match
Best Local Sim
Matches 73;

Similarity

100.0%;

Score 73; DB 6; Pred. No. 6.2e-06; 25 G; 72 T; 0 U;

Conservative

0

Mismatches

0

0

Gaps

0

Sequence 245

BP; 101 A; 40 C;

7 Other, Length Indels

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RESULT 3
ABV94414/c
ID ABV944
XX Breast
XX Breast
XX W 88
XX W 88
XX W 88
XX W 802002
XX 07-DEC
XX 07-DEC
XX 07-DEC
XX 07-DEC
XX 07-DEC
XX NOVEL
PH Carcin
PH Subseq
PH Carcin
PH Subseq
PH Calls.
XX Claim

                                                                                            CC polynuclectide sequences chosen from the 468 sequences given in ABV94010
CC to ABV94477. Also described: (1) a polynuclectide array (II) useful for the prognosis or diagnostic of tumour, comprising (I); and (2) detecting CC (MI) differentially expressed polynuclectide sequences which are CC excrelated with a cancer, involves obtaining a polynuclectide sample from CC a patient, and reacting the polynuclectide sequences which are proposed immobilised on a solid support, where the probe comprises any combination CC of the polynuclectide sequences of (I) or its expression products encoded by polynuclectide sequences of (I), and detecting the reaction product. (CC (I) have cytostatic activities and can be used as anti-tumour agents. (I) is useful in molecular characterisation of a carcinoma. (I) and (II) are CC useful for the prognosis or diagnostic of tumour, in differentiating a cancer cell, detecting a hormone sensitive tumour CC cll, differentiating a tumour with lymph nodes from a tumour without CC lymph nodes, differentiating antracycline-sensitive tumours from CC cancer treatment, and for detecting differentially expressed genes that CC cancer treatment, and for detecting differentially expressed genes that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ß. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a polynucleotide library (I) useful the molecular characterisation of a carcinoma, comprising a pool of polynucleotides or its subsequences which are either underexpressed overexpressed in tumour cells, and correspond to any of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide library useful in molecular characterization of a carcinoma, comprising a pool of polynucleotide sequences or its subsequences which are either underexpressed or overexpressed in tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-2000;
07-DEC-2001;
                                                                              correlated with a cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-619023/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bertucci F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001WO-IB002811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast carcinoma related nucleotide sequence SEQ ID NO:405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 364; 401pp; English.
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RESULT 4
ACH22964
ID ACH22964
ACH22964
ACH22964
ACH22964
ACH22
ACC ACH2
ACC AC
                                                                                                                                                                    The invention relates to an isolated polynuclectide comprising any one of CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was Cd determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for CC identifying expressed genes or for physical mapping of the human genome, CC in forensics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide Sequences are also useful as hybridisation probes, as oligomers for PCR, CC for chromosome and gene mapping, in the recombinant production of protein, or in generating antisonse DNA or RNA. The purified polypeptide is useful for generating antisonse DNA or RNA. The purified polypeptide is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data CC is one of the solated cDNA/EST sequences. Note: The sequence data CC obtained in electronic format directly from USPTO at Sequence in the state of the printed specification, but was CC sequence in the properties of the printed specification, but was CC sequence in the printed specification, but was considered to the printed specification, but was constant diameter. The sequence constant diameter. The sequence constant diameters are sequence.
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Query Match
Best Local S
Matches 73
                                                                                                                          Sequence 465 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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(STAC/)
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                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) LABAT I.
) STACHE-CRAIN B.
) DICKSON M C.
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mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JONES L W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 10176; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGTTTTATTGTGTTTTTAATTTATTTAAGATGGATTCTCAGATATTTATATTTTT
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                                                                                                                       146 A; 58 C;
                             100.0%;
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                             Score 73; DB 8;
Pred. No. 5.8e-06;
                                                                                                                          74 G; 169 T; 0 U; 18 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dickson MC,
                                                      Length 465;
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Conservative

0; Mismatches

Indels

0

Gaps

0

59 G;

144 T; 0 U; 1 Other;

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ABZ35131/c
ABZ35131;
XX
ABZ35131;
XX
ABZ35131;
XX
O5-FEB-2003 (first entry)
XX
Human gene expression profile p
XX
Human; arrery; endothelium; unt
XW
Human; arcrory; endothelium; prostate;
XW
Human; arcrorarray; geneme mapp
XX
Homo sapiens.
XX
OS Homo sapiens.
XX
Y
Y
Y
20-MAR-2002; 2002WO-US008456.
XX
20-MAR-2001; 2001US-0276947P.
XX
Y
XX
ORTH) ORTHO CLINICAL DIAGNOS;
XX
(ORTH) ORTHO CLINICAL DIAGNOS;
XX
(ORTH) ORTHO CLINICAL DIAGNOS;
XX
Y
PH
XX
(ORTH) ORTHO CLINICAL DIAGNOS;
XX
Claim 7; Page 427; 850pp; Engl:
XX
PF pathologies involving alteratic
XX
Claim 7; Page 427; 850pp; Engl:
XX
Claim 7; Page 427; 8
                                                                                                               The invention relates to a gene expression profile comprising one or more CC genes (ARZ34889-ARZ35692) and generated from a cell type. The cell type can be a coronary artery endothelium, umbilical artery or vein endothelium, coronary artery endothelium, umbilical artery or vein endothelium, coronary artery endothelium, prometrium microvascular endothelium, keratinocyte coronary endothelium, prostate epithelium, renal epithelium, prostate epithelium, prostate epithelium, renal proximal tubule epithelium, coronary artery smooth muscle, mesangial cells, coronary artery smooth muscle, astrocytes, coronchial fibroblast, neural progenitor cells, skeletal muscle, astrocytes, coronchial smooth muscle, mesangial cells, coronary artery smooth muscle, coronchial smooth muscle, mesangial cells, coronary artery smooth muscle, coronchial smooth muscle, mesangial cells, coronary artery smooth muscle, coronchial smooth muscle, mesangial cells, coronary artery smooth muscle, coronchial smooth muscle, astrocytes, coronchial smooth muscle, mesangial cells, coronary artery smooth muscle, set contains the level of RNA expression for a sample, determining the coronary of a cell and distinguishing cell types. The gene or a profile may repression profile is useful in identifying disease pathologies involving calterarions of gene expression. The assessment of expression profile may also be used for creating microarrays. The microarray is useful for centic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue cidentifications and in identifying promising antibiotics, antiviral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 427; 850pp; English.
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RESULT 6
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XX ADE849
XX ADE849
XX Ss; Cy
KW Ss; Cy
KW Guinol
XX Homo s
PN WO2003
XX Homo s
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                                                                                                            Query Match
Best Local S
Matches 73
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1-H-inidazol-5-yl)methyl)-4-(3-chlorophenyl)-1-methyl-2-(H)quinolinone, monitoring the therapy of a patient treating a patient with leukemia with FTI if the analysis indicates that the patient with leukemia with FTI if the analysis indicates that the patient with leukemia with FTI if the corresponds to a gene whose expression may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
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30-OCT-2001; 2001US-0340031P.
30-OCT-2001; 2001US-0340938P.
30-OCT-2001; 2001US-0341012P.
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 197; 346pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-513497/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-2002; 2002WO-US034784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quinolinone; leukemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Farnesyl transferase inhibitor modulated leukemia associated gene. #197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004
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                                                                                                                                                                                                                                                                                modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORTH ) ORTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; farnesyl transferase inhibitor; gene expression;
     189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                            Similarity 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        μ
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     AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT
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                                                                                                         100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                        BP;
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                                                                                                                                                                                                                           188
                                                                                                                                                                                                                           A; 85 C;
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•
                                                                                                      Score 73; DB y; Pred. No. 5.8e-06;
                                                                                                                                                                                                                           59 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB 6;
Pred. No. 5.8e-06;
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                                                                                                                                                                                                                        144 T; 0 U; 1 Other;
                                                                                                                                                                 Length 477;
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                                                                                                               Indels
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                                                                                                               Gaps
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130
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                                                                                                         Matches
                                                                                                                                   Query Match
                                                                                                                                                                                     This invention relates to the sequences of several cDNAs that are differentially expressed in activated T cells. The sequences of the invention may have antiallergic, cytostatic, immunosuppressive and antimicrobial activity and may be used in gene therapy. The invention also comprises a method for screening samples for differentially expressed genes and a method for detecting these cONAs by hybridisation. The methods and compositions of the present invention are useful for diagnosing, treating, staging or monitoring treatment for allergy, cancer, chronic graft versus host disease, infectious and/or autoimmune disorders. The present sequence represents a cDNA of the invention that is differentially expressed in activated T cells
                                                                                                                                                                                                                                                                                                                                                                                                 New combination comprising several cDNAs that are differentially expressed in activated T cells, useful for diagnosing, treating, or monitoring treatment for allergy, cancer, infectious and/or a
                                                                                                                                                              Sequence 1176 BP; 307 A; 266 C; 270 G; 333 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T cell; gene; ss; differential expression; T cell activation; antiallergic; cytostatic; immunosuppressive; antimicrobial; gallergy; cancer; graft versus host disease; infection;
                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                       disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hopkins CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAWK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOPK/) HOPKINS C M.
                                                                                                                        Local
1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PETERSON D P. COCKS B G. HAWKINS P R.
                                                                                                                        Similarity
                           ATTTTATTTTTT 73
                                                                                AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 60
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                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peterson DP,
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                                                                                                                      100.0%;
                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cocks BG,
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                                                                                                         0;
                                                                                                        Score 73; DB
Pred. No. 5.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hawkins
                                                                                                                        5.2e-06;
                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR;
                                                                                                                                   Length 1176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                        Gaps
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RESULT 8
ADD29870
ID ADD29870
ID ADD29870
AC ADD2
XX ADD2
XX BS;

AAI13509
ID AAI1
XX
AC AAI1
XX
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                                                                                                                                                    RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for diagnosing a cancer in a subject. the method comprises determining, in a sample from the subject, the level of at least one polypeptide, where a higher level of the cancer is indicative of the level of the polypeptide in a subject free of cancer is indicative of cancer. The polypeptide is selected from any of the polypeptides encoded by the polypeptides listed in the specification and polypeptides which are at least 70% homologous to the polypeptides. The method of the invention has cytostatic activity, and markers specific for one or several types of cancer, depending on the tissue origin, which may be used in numerous diagnostic and prognostic applications as well as cancer type-specific targets for therapeutic intervention. The compounds that modulate the activity of a tumour suppressor gene are useful in the treatment of cancer or as anti-cancer drugs. The present sequence represents a polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                  AAI13509,
                                                                                           AAI13509 standard; DNA; 1946 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing cancer comprises determining the polypeptide or polynucleotide levels e.g., hepatic lipase, in a sample from a subject, where a higher level compared to that in a subject free of cancer is indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 301; 272pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (QUAR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumour suppressor mRNA
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                                                                                                                                                                                                                                            1797
                                                                                                                                                                                                                                                                                                                                                                 1737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                                                                                                                                                                                                       <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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CLEVELAND CLINIC FOUND
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                                                                                                                                                                                                                                                                                                  ATTTTATTTTTT 73
                                                                                                                                                                                                                                                                                                                                                           AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 1796
                                                                                                                                                                                                                                            ATTTTATTTTTT 1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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RESULT 10
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Best Local S
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-GSP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeIa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn
                       Human; foetal
                                                 Human foetal liver single exon nucleic acid probe #3512.
                                                                            01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                        Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                     ABA55207;
                                                                                                                              ABA55207 standard; DNA; 1946 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #3442 for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                               1639
                                                                                                                                                                                                                                                  1579 AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                 human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                              ATTTTATTTTTTT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3442; 487pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                          (first entry)
                      liver; gene expression; single exon
                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                  5e-06;
                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                               Length 1946;
                        nucleic
                                                                                                                                                                                                                                                                                                      Indels
                      acid probe;
                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                  1638
                                                                                                                                                                                                                                                                           60
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Homo sapiens

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RESULT 11
AAI34869
ID AAI344
XX AAI34
XX AAI34
XX Probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 04-FEB-2000;
26-MAY-2000;
                                                                                                     WO200157272-A2
                                                                                                                                                             genetic disorder;
                                                                                                                                                                            Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                     Probe #3555 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                    17-OCT-2001
                                                                                                                                                                                                                                                                                             AAI34869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3512; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000669.
                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                      1639
                                                                                                                                                                                                                                                                                                                                                                                                                             1579
                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG
                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGTTTTATTGTGTTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT
                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                  ATTTTATTTTTTT 73
                                                                                                                                                                                                                                                                                                                                                                    ATTITATTTTTTT 1651
                                                                                                                                                                                                                                                                                                                                                                                                                             AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT
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2000US-0207456P.
2000US-0068408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
2000US-0180312P.
2000US-0207456P.
                                           2001WO-US000663
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                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                             1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a single exon nucleic acid probe for measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 12
ABA44752
ID ABA44
XX ABA44752
AC ABA44
XX Human
DT 01-FE
XX Human
XX Human
XX Human
XX Homo

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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.
                          WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000662.
                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA44752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA44752 standard; DNA; 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AACGTTTTATTGTGTTTTTAATTTAATTTAATATTAAGATGGATTCTCAGATATTTATATATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTATTTTTT 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTATTTTTT
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                                                                      Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO. 3555; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                             ; 2000US-0180312P.
2000US-0207456P.
; 2000US-020608409.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0234359P.
; 2000GB-00024263.
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                                                                        DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single exon nucleic acid probe #3447.
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                                                                           Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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Pred. No. 5e-06;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR
                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression; breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
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RESULT 13
ABA24954
XX
ABA24954
XX
ABA24454
XX
AC ABA24
XX
DT 23-JA
XX
Probe
XX
Human
KW cardi
KW conge
XX
Homo
XX
Homo
XX
O9-AU
XX
30-AU
PF 30-JU
PR 30-JU
PR 30-JU
PR 30-JU
PR 31-SE
PR 21-SE
PR 21-SE
PR 21-SE
PR 21-SE
PR 04-OC
XX
POLB
PR 10-OC
XX
POLB
XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA24954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #3420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA24954 standard; DNA; 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1639
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                                                                        MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTITATTTTTT 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGTTTTATTGTGTTTTTAATTTATTTAAGATGGATTCTCAGATATTTATATATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTTATTTTTT
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Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                         2000GB-00024263.
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100.0%; )
tive 0;
Chen W, Rank DR;
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Pred. No. 5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 14
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AC AAX28
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                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
04-OCT-2000; 2000GB-0004263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                        WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nearts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th 100.0%; Similarity 100.0%; 73; Conservative 0;
                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTTATTTTTT 1651
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                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marrow expressed single exon probe
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                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DE
Pred. No. 5e-
0; Mismatches
                                                                                                                                                              Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Human genome-derived single exon nucleic gene expression in human bone marrow.

acid probes useful for analyzing

gene expression

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RESULT 15
RAK03468
ID AAK03468
ID AAK03468
AC AAK03
AC AAC03
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AC AAC04
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-483446/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe SEQ ID NO: 3459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK03468 standard; DNA; 1946
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                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 3459; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO 3479; 658pp + Sequence Listing; English.
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
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Best Local !
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                                                          1 AACGTTTTAITGTGTTTTTAATTTATTTAAGATGGATTCTCAGATATTTATATTTTT 60
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                                            ACCTTTATCTCTTTTATTTATTTATTAACATGCATCTCAGATATTTATATATTTT
                       ATTTTATTTTTT
ATTTTATTTTTT 1651
                                                                                                          100.0%; Score 73; DB 4; Length 1946; 100.0%; Pred. No. 5e-06;
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Search completed: October 14, 2004, 17:30:27 Job time : 288 secs

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Result
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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PCT-US93-06251-20
US-09-702-705-579
US-09-702-705-579
US-09-702-705-579
US-09-704-457-571
US-09-614-124B-579
US-09-614-124B-579
US-09-671-325-579
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US-09-689-184-579
US-09-689-184-579
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Sequence 70, Appl
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Sequence 34, Appl
Sequence 34, Appl
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45.8	45.8	45.8	46.0	46.0	46.3	46.3	46.3	46.3	46.3	46.6	46.8	46.8	46.8	47.1	47.1	47.1	47.1
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Sequence 1294, Ap	Sequence 73, Appl	Sequence 1325, Ap	Sequence 13, Appl	Sequence 80, Appl	Sequence 24, Appl		Sequence 50, Appl	Sequence 11, Appl	Sequence 1878, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 16138, 1	Sequence 1, Appl:	Sequence 2, Appl:	Sequence 1, Appl:	Sequence 71, Appl

ALIGNMENTS

### US-08-306-691B-44 RESULT 1 US-08-306-691B-44 Sequence 44, Application US/08306691B Patent No. 5734039 GENERAL INFORMATION: APPLICANT: Calabretta, Bruno APPLICANT: Calabretta, Bruno APPLICANT: Storiski, Tomasz TITLE OF INVENTION: ANTISENSE TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES TELEFAX: (215) 568-554 TELEX: No. 5734039e INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3565 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: lines-APPLICATION NUMBER: US/08/306,691B FILING DATE: September 15, 1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: COMPUTER: IBM PS/2 OPERATING SYSTEM: MS-DOS SOFTWARE: WORDPEFFECT 5.1 CURRENT APPLICATION DATA: COUNTRY: U.S.A. ZIP: 19102 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, ATTORNEY AGENT INFORMATION: NAME: MODACO, Daniel A. REGISTRATION NUMBER: 30,480 REFERENCE/DOCKET NUMBER: 83 TELECOMMUNICATION INFORMATION: CORRESPONDENCE ADDRESS ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Two Penn Center, Suite 1800 CITY: Philadelphia STATE: Pennsylvania TELEPHONE: : (215) 568-8383 (215) 568-5549 8321-8 720 8

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1 AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 60

Query Match Best Local Similarity Matches 73; Conserv

100.0%; Score 73; DB 1; 100.0%; Pred. No. 1.4e-08;

Length 3565;

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Mismatches

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RESULT 3
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PCT-US93-06251-20
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/ACCURATION:
                                                                                                          Sequence 571, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 856
REERRENCE/DOCKET NUMBER: 856
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPAX: 516-742-4366
TELEPAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                         APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
                                                                                                                                                                                                                                                                                                                                                                                                      Local
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   Panger, Gary
Vedvick, Tom
Carter, Darrick
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                                                        Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                         Wang, Tongtong
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100.0%; Pred. No. 1.4e-08;
A. Mismatches 0;
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Trivalent Synthesis of Oligonucleotides Containing
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CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 571
RESULT 5
US-09-736-457-571
; Sequence 571, Application US/09736457
; Patent No. 6509448
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US-09-702-705-579
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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INTENTION.
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILLING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Manni
APPLICANT: Fan,
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 40
TYPE: DNA
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                                                                                                                                                                                   225 AACGITTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATT
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                                                                                                                                               61 ATTTTATTTTTT 73
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Similarity 98.6%;
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Bangur, Chaitar
Lodes, Michael
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Mannion, Jane
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Pred. No. 3.4e-08;
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Pred. No. 3.4e-08;
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GENERAL INFORMATION:

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; SOFTWARE: FastSEQ for I
; SEQ ID NO 579
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-579
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APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION UNMER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 571
LENGTH: 402
TYPE: DNA
ORGANISM: Homo sapien
US-09-736-457-571
                                                                                                                                                                                                                                                                                                   APPLICAN: Bangur, Chaitanya ...
APPLICANT: Bangur, Chaitanya ...
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: 210121.478C15
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Best Local Similarity
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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les 72; Conserv
225 AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTT
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                   1 AACGITTTATIGTGTITTTAAITTATITATTAAGAIGGATTCTCAGAIATTTTATATTTT 60
                                                                              72; Conservative
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Carter, Darrick
Retter, Marc
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Bangur, Chaitanya S.
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Lodes, Michael A.
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                                                                              Score 71.4; DB 4; Length 402; Pred. No. 3.4e-08; 0; Mismatches 1; Indels
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284
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APPLICANT: Panger, Garry
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 571
LENGTH: 402
                                                                                                                                                                       APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.47869
CURRENT APPLICATION UNMBER: US/09/614,124B
CURRENT APPLICATION UNMBER: US/09/614,124B
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 579
                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-1248-579
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; ORGANISM: Homo sapien
US-09-614-124B-571
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Query Match 97.8%; Score 71.4; DB 4; Best Local Similarity 98.6%; Pred. No. 3.4e-08; Matches 72; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 579, Application US/09614124B Patent No. 6630574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 97.8%; Score 71.4; DB 4; Best Local Similarity 98.6%; Pred. No. 3.4e-08; Matches 72; Conservative 0; Mismatches 1;
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APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
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                                                                                                                                                           LENGTH: 402
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Lodes, Michael
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Indels

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Gaps

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APPLICANT: Retter, Marick
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Pan, Liqun
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITILE OF INVENTION: DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT APPLICATION NUMBER: US/09-26
NUMBER OF SEQ ID NOS: 1825
SOPTWARE: PastSEQ for Window-
SEQ ID NO 579
LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 571
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-571
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GENERAL INFORMATION:
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TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILLING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: F
APPLICANT: F
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mes 72; Conservat
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Vedvick, Tom
Carter, Darrick
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Bangur, Chaitanya
Lodes, Michael A.
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Pred. No. 3.4e-08;
0; Mismatches 1;
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RESULT 12
US-09-589-184-579
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TYPE: DNA
ORGANISM: Homo sapien
US-09-589-184-571
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                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Wang, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: F
SEQ ID NO 571
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APPLICANT:
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                                                                                                                                                                                                                                   Sequence 579, Application US/09589184 Patent No. 6686447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity 98.6%;
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APPLICANT:
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APPLICANT:
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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 668644
             APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
CURRENT APPLICATION NUMBER: US/09/589,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 97.8%;
Local Similarity 98.6%;
les 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            225 AACGTTTTATTGTGTTTTTAATTTTATTTATAAGATGGATTCTCAGATATTTATATTTTT 284
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                                                                                                                                                            Bangur, Chaitanya
Lodes, Michael A.
                                                                                                                                                                                                  Wang, Tongtong
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Lodes, Michael A.
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Bangur, Chaitanya S.
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                                                                                                                                                                                 Chaitanya S.
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Pred. No. 3.4e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71.4; DB 4;
Pred. No. 3.4e-08;
0; Mismatches 1;
                                                     FOR THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 402;
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61 UAUUUUUUU 69

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; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDENESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
US-08-146-421-2
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US-08-146-421-2
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                                                                                                          Query Match
Best Local Similarity
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No. 5543499
                                                                                                 Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,421
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
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Best Local
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                               TELEFAX: 619-453-2839 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: F
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TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PEPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 489-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: DNA
TITLE OF INVENTION: ANT
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65 TATTTTTT 73
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                             OO DUUAUUUUUUAAUUUAAUUUAAUUAAGAUGGAUUCUCAGAUAUUUAUAUUUUUUAUAUUU 60
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4350 LA JOLLA VILLAGE DRIVE, SUITE 300
                                                                                                Conservative
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                                                                                          94.5%; Score 69; DB 1; Le 34.8%; Pred. No. 1.2e-07; tive 45; Mismatches 0;
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Pred. No. 3.4e-08;
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                                                                                                                           Length 69;
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                                                                                              Indels
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; FEATURE: ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-70
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CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
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Query Match
Best Local Similarity
                                                                                                                                                                                                   SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 70, Appl. Patent No. 667773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Patent No. 6627398
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TITLE OF INVENTION: SYSTEM FOR REPRODUCING AND MODULATING STABILITY AND
TITLE OF INVENTION: TURNOVER OF RNA MOLECULES
FILE REFERENCE: 601-1-080N
CURRENT APPLICATION NUMBER: US/09/320,609
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: US 60/086,675
EARLIER PILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OLEK,
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                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: By hybridizing OTHER INFORMATION: this synthetic oligonucleotide and its appropriate OTHER INFORMATION: complement , templates for Fos-AO RNA were OTHER INFORMATION: generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                         ENGTH: 6040
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TYPE: DNA
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    51.8%;
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    Score 37.8; DB Pred. No. 0.86;
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0.32;
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                       Length 6040;
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Search Job ti	Дb	Ş	Дb	Ś	Matches
Search completed: 'Job time : 69 secs	1818	61	1758	_	
Bed	11-	-A	A-	-≱	1,
Search completed: October 14, 2004, 18:42:43	1818 TTTTTTAATTT 1830	61 ATTTTATTTTTT 73	1758 AATTTATATTTTATTTTTATTTGTTTAGTAGTAGTTTTTT	AACGTTTATTGTGTTTTTAATTTTATTTATTAAGATGGATTCTCAGATATTTATATATTTT	51; Conservative
004,	0		TTAI	TAAT	0;
18:42:43			TTGTTTAGTTAG	TTATTTATTAAG	0; Mismatches
			AGTTI	TGGAT	22;
			TTTAAGATT	TCTCAGATA	22; Indels
			LITIT	TTAT	0,
			ATTTTT	ATTTTT	0; Gaps
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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07
2: /cgn2_6/ptodata/1/pubpna/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                 _6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

14	13	12	11	c 10	ø	8	c 7	6	G U	4.	w	N	_	Result No.
73	73	. 73	73	73	73	73	73	73	73	73	73	73	73	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query
265	265	255	255	245	240	240	239	239	239	237	237	75	73	Query Match Length
16	13	16	13	15	16	13	15	14	φ	16	13	17	17	DB
US-10-242-535A-19213	US-10-085-783A-19213	US-10-242-535A-893	US-10-085-783A-893	US-10-007-926A-405	US-10-242-535A-30739	US-10-085-783A-30739	US-10-146-502-1169	US-10-046-935-1169	US-09-878-178-1169	US-10-242-535A-34451	US-10-085-783A-34451	US-10-658-093-14	US-10-658-093-19	ID
	Sequence 19213, A			Sequence 405, App	Sequence 30739, A		Sequence 1169, Ap	Sequence 1169, Ap	Sequence 1169, Ap	Sequence 34451, A	Sequence 34451, A	Sequence 14, Appl	Sequence 19, Appl	Description

RESULT 2 US-10-658-093-14

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	c 21		19	18	17	16	: !
71.4	71.4	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	
97.8	97.8	100.0	100.0	100.0		•	٠	100.0	100.0	100.0	100.0	100.0	100.0	•	100.0	100.0	•	100.0	100.0	100.0	100.0	•	•	100.0	•	٠	•	100.0	•	
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US-09-736-457-579	US-09-736-457-571	US-10-087-192-1594	US-10-775-169-188	-10-717-597-	-464-	-10-101-510-	-10-	US-09-968-007A-433	US-09-873-367C-793	US-09-873-319-649	US-09-960-706-993	US-10-106-698-289	US-09-925-299-129	US-09-925-299-129	US-10-002-600-36	US-10-264-049-347	US-10-116-802-292	US-09-971-392-8	US-10-341-434-173	US-10-007-926A-318	US-09-864-761-3420	US-10-062-674-2057	•	US-10-283-975A-197	-10-101-		-10-242-535A	US-10-085-783A-29586	242-535A-	
Sequence 579, App	571,	1594	188,	141,	135,	201	127	433	Sequence 793, App	649	993	289	e 129,		36,	347	29		17	e 31	342	20	е 39	Sequence 197, App	24	e 10176,	e 29586,	Sequence 29586, A	26860,	0 20000

### ALIGNMENTS

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US-10-658-093-19

# Sequence 19, Application US/10658093

# Publication No. US20040115704A1

# GEMERAL INFORMATION:

APPLICANT: Daly, John Michael

# TITLE OF INVENTION: Constructs for Gene Expression Analysis

# FILE REFERENCE: 12177722

# CURRENT APPLICATION NUMBER: US/10/658,093

# CURRENT FILING DATE: 2003-09-09

# PRIOR APPLICATION NUMBER: US/10/674770

# PRIOR APPLICATION NUMBER: US/10/0351

# PRIOR APPLICATION NUMBER: PCT/AU02/00351

# PRIOR FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                    US-10-658-093-19
                                                                                                                                                                                                                                                                                          ; SEQ ID NO 19
; LENGTH: 73
; TYPE: DNA
                                                                                                                                                                                       Best
                                                                                                                                                                 Matches
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                      ORGANISM: mammalian
                                                                                                                                                            y Match 100.0%; Score 73; DB 17; Local Similarity 100.0%; Pred. No. 1.1e-06; hes 73; Conservative 0; Mismatches 0;
61
                                     61 ATTITATITITIT 73
                                                                             Length 73;
                                                                                                                                                              Indels
                                                                                                                                                              0,
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RESULT 4
US-10-242-535A-34451
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                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-34451
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; ORGANISM: mammalian
US-10-658-093-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34451, Application US/10085783A Phiblication No. US20040037841A1 GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2
SEQ ID NO 34451
LENGTH: 237
                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liew, C.C.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Daly, Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/10658093
Publication No. US20040115704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/658,093
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: USSN 60/274770
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: PCT/AU02/00351
PRIOR APPLICATION NUMBER: PCT/AU02/00351
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Constructs for Gene Expression Analysis FILE REFERENCE: 12177722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                           61 ATTTTATTTTTT 73
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                                                                                                                                                                                              AACGITTTATIGIGITTTTTAATITTATTAAGAIGGATTCTCAGAIATTTATATTTTT 60
                                                                                                                                                                      ÄACGTTTTÄTTGTGTTTTTÄATTTATTTÄTTÄAGATGGATTCTCAGÄTATTTÄTATÄTTTT 121
                                                                                   ATTTTATTTTTT 134
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                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
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Pred. No. 1.4e-06;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                          Length 237;
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61 ATTTTATTTTTT 73

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APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: Feature for Windows Version 4.0
SEQ ID NO 1169
LENGTH: 239
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(239)
OTHER INFORMATION: n = A,T,C or G
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CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1169, Application US/09878178 Patent No. US20020177552A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34451, Application US/10242535A

Publication No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

APPLICANT: Liew, C.C.

FILE REFERENCE: 4231/2005

FILE REFERENCE: 4231/2005
                                                                                   Matches
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LENGTH: 237
                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 58994
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  190 AACGITITATIGIGITITIAATIT
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                                                                                   73;
                                        1 AACGITTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 60
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                                                                                 h 100.0%; Score 73; DB 9; 1
Similarity 100.0%; Pred. No. 1.4e-06;
73; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.0
tive 0; Mismatches
  1.4e-06;
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                                                                                                                            Length 239;
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OTHER INFORMATION: n = A, T, C or G US-10-146-502-1169
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; LOCATION: 223
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-046-935-1169/c
                                                                                                                                                                                                                                                            FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1169
    Query Match 100.0%; Score 73; DB 15; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 73; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1169, Application US/10146502 Publication No. US20030069180A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1169
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jiang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.527C1
                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 223
                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                            ENGTH: 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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Wang, Aijun
Stolk, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                    Length 239;
Indels
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Gaps
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; LENGTH: 240
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-30739
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                                                         SOFTWARE: Pater
SEQ ID NO 30739
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30739, Application US/10242535A Publication No. US20040013663A1 GENERAL INFORMATION:
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                                                                                                                       TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/375,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-02-28
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                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/085,783A CURRENT FILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: US 60/305,340 PRIOR FILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: US 60/275,017 PRIOR FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/271,955 PRIOR FILING DATE: 2001-02-28
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TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
                                      ENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ATTTTATTTTTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATTTTATTTTTT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AACGITITATTGTGTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACGTTTTATTGTGTTTTTAATTTÄTTTÄTTTAAGATGGATTCTCAGATATTTÄTÄTTTTT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 73; DB 13; 100.0%; Pred. No. 1.4e-06; O; Mismatches O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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US-10-007-926A-405/c
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                              LOCATION: (242)
OTHER INFORMATION: a, t, c or 3-10-007-926A-405
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 405
LENGTH: 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
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OTHER INFORMATION: a, t,
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
                                                                                                       OTHER INFORMATION: a, t, c
                                                                                                                                                                       OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                 LOCATION: (230)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                               FEATURE:
                                                                                                                                    NAME/KEY: modified_base
                                                                                                                                                                                          NAME/KEY: modified_base 
LOCATION: (237)
                                                                                                                                                                                                                                   OCATION: (234)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                 OCATION: (223)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified_base
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                                                                           AME/KEY: modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
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                                                                                                                             (240)
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100.0%; Score 73;
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Pred. No. 1.4e-06;
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DB 15;
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Length 245;
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APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
ITILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR PRIOR DATE: 2001-03-12
PRIOR PILING DATE: 2001-02-28
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; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-893
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                                                                                                                                                                                                                                                                                                                                          Sequence 893, Applic Publication No. US20 GENERAL INFORMATION:
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SEQ ID NO 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
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OF SEQ ID NOS:
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o. US20040013663A1
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nilarity 100.0%;
Conservative 0
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5. US20040037841A1
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Pred. No. 1.4e-06;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
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; LENGTH: 265
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-19213
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                                                                                                                                                                                                                         Sequence 19213, Application US/10242535A publication No. US20040013663A1 GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 19213
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PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR EILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
                                                                                                                        APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
CURRENT FILING DATE: 2002-09-12
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TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
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Pred. No. 1.4e-06;
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RESULT 15 US-10-085-783A-26860

GENERAL INFORMATION

APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.

Sequence 26860, Application US/10085783A Publication No. US20040037841A1

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145 ATTTTATTTTTT 157

61 ATTTTATTTTTT 73

85 AACGTTTTATTGTGTTTTTAATTTATTTATATATAGATGGATTCTCAGATATTTATATTTTT 144

AACGTTTTATTGTGTTTTTAATTTATTATTATAGATGGATTCTCAGATATTTTATATTTTT 60

US-10-242-535A-19213

TYPE: DNA
ORGANISM: Human

ENGTH: 265

Matches Best Local Query Match

73; μ

Similarity

100.0%; illarity 100.0%; Conservative 0

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Score 73; DB 16; Pred. No. 1.4e-06; Mismatches 0;

Length 265;

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; PRIOR FILING DATE: 2 ; NUMBER OF SEQ ID NOS ; SOFTWARE: PatentIn v ; SEQ ID NO 19213

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Search completed: October 14, 2004, 19:34:13
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Query Match

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SOPTWARE: PatentIn version 3.2 SEQ ID NO 26860

LENGTH: 281
TYPE: DNA
ORGANISM: Human

FEATURE:

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994

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Result
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 BE827983
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BE827983 RC4-ET002
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R79209 Y188b05.81
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AUTHORS
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BE827983
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466312 731700	1 CB46631	N	8	73
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754739 208340	3 BE75473	$\mathbf{r}$	8	73
091171 BX09117	3 BX09117	$\boldsymbol{\vdash}$	8	73
6497 yz44b03	4 N6649	മ	8	73
21936 d£30£04.	AW0219	മ	ë.	73
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20879 ze64g03.	AA0208	4	0	73

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 183)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 183 bp mRNA linear EST 22-SEP-2000 ET0024 Homo sapiens cDNA, mRNA sequence.

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REFERENCE
AUTHORS
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Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 214)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J., Kenty, G., Gradwohl, G., Clifton, S., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC4-ET0024-290
500-013-e10&t3=2000-05-29&t4=1)
Seg_primer: puc 18 forward
User_primer: puc 18 forward
                                                                                                                                                                  Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
MA 02138
                                                                                                                          Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                               Endocrine Pancreas Consortium 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: +55-11-2707001
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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/dev_stage="Adult"
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Pred. No. 0.007;
; Mismatches 0;
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                                                                                                                                                                                              . Institute
/ Divinity &
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: 3', mRNA
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RESULT 3
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DEFINITION
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VERSION
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Query Match
Best Local S
Matches 73
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216)

Fujiwara T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takadichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.

Fujiwara et al. (1995)

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
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D58202.1 GI:964824
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D58202 216 bp mRNA linear EST 28-AUG-19 HUM355D05B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-355D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -40UP from Gibco
High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
05suka Pharmaceutical cho.,Ctd
463-10 kagasuno Kawauchi-cho,
Tel: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
h 100.0%; i
Similarity 100.0%; i
73; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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llarity 100.0%;
Conservative 0
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/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript site."
/note="Torgan: Pancreas; Vector: pBluescript site."
/note="Torgan: Pancreas; Vector: pBluescript site."
/note: State is a sparose gel. Average insert size."
/note: State was destroyed after directional cloning.
/note: Amplified once. Contact information: Hiroshi Inoue, MD,
/note: Amplified once. Contact information: Hiroshi Inoue, MD,
/note: Metabolism Div. (Alan Permutt Lab), Washington University
/note: State is a sparose st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsutomu Fujiwara
                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-355D05"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Purified pancreatic islet"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:"
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/db_xref="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                              .216
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                                Score 73; DB 14;
Pred. No. 0.0063;
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Pred. No. 0.0064;
); Mismatches 0;
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                                                                    DB 14;
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                                                                    Length 216;
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R79209/c
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155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
Contact: Wilson RK
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1800
Pax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
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                                                                 h 100.0%; Score 73; DB 14;
Similarity 100.0%; Pred. No. 0.0059;
73; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
Insert Size: 800
High quality sequence stops: 241
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 800 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R79209 243 bp mRNA linear EST yi88b05.sl Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146289 3' similar to gb:V01512_rna5 P55-C-FOS PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: Promega -21ml3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AACGITTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 96
                   AACGTTTTATTGTGTTTTTAATTTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 241.
                                                                                                                                                                        constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:146289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                       sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="GDB:557815"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           School of Medicine way, Box 8501, St. Louis, MO 63108
                                                                     ç
                                                                                                      Length 243;
                                                                   Indels
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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AA020879/c
LOCUS
ORIGIN
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JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiapes, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, Mardis, B., Moore, B., Morris, M., Parsons, J., Prange, G., Rifkin, L., Mardis, E., Moore, B., Morris, M., Parsons, J., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28M13 rev2 from Amersham High quality sequence ston: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSET Length: 2316 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA020879

245 bp mRNA linear EST 30-JAN-199:
ze64g03.rl Soares retina N2b4HR Homo sapiens cDNA clone
zmAGE:363796 5' similar to gb:V01512_rna5 p55-C-FOS pROTO-ONCOGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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314 286 1810
           /tissue_type="retina"
/dev_stage="55 year_old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="GDB:1280499"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                        sex="male"
                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:363796"
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Query Match 100
Best Local Similarity 100
Matches 73; Conservative

100.0%; Score 73; DB 9; 100.0%; Pred. No. 0.0058; tive 0; Mismatches 0

DB 9; Length 245; 0

Indels

0

Gaps

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REFERENCE
AUTHORS
TITLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 284)

Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takadichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)

L Unpublished (1995)

Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-55-2888
                                                                                                                                                                                                                                                                                                                                                                                            122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmeri,D., Zhou,R.-R., Rosen,S.D. and Hemmerich,S. Gene expression profiling of peripheral lymph node addressin+ high endothelial venule cells from human tonsil: implications in lymphocyte recirculation and inflammation
                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 291)

Palmeri,D., Zhou,F.-R., Rosen,S.D. and Hemmerich,S.
                                                                                                                                                                                                                                                                  BM955729 291 bp mRNA linear EST 30-SEP-2002 EST0664 HEV PCR-select Homo sapiens cDNA clone HEV#1046 similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D57391 284 bp mRNA linear EST 28-AUG-1:
HUM299H07A Clontech human aorta polyA+ mRNA (#6572) Homo sapiens
CDNA clone GEN-299H07 3', mRNA sequence.
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Similarity 100.0%;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="GEN-299H07"
'clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
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Pred. No. 0.0053;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATTITATTITTT 73
                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 331)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AACGITTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT
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Contact: Rosen SD
Department of Anatomy
University of California at San Francisco
HSW-1120, 513 Parnassus Ave., San Francisc
Tel: 415 476 1579
Fax: 415 476 4845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF436565 331 bp mRNA linear EST 29-NOV-2000 7515603.x1 NCI_CGAP_Br22 Homo sapiens cDNA clone IMAGE:3645845 3',
                                        info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 308.
Location/Qualifiers
                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="high endothelial"
/clone lib="HEV PCR-select"
/clone lib="HEV PCR-select"
/note="Torgan: tonsil; Vector: pCRII; Site_1: EcoRI;
/site_2: EcoRI; High endothelial cells (HEC) were isolated
from human tonsils using magnetic beads derivatized with
MECA-79 antibody specific to the peripheral lymph node
addressin. cDNA was prepared from these cells using
cap-Finder methodology, then cDNA prepared from tonsillar
lymphocytes and from human umbilical vein endothelial
cells were subtracted from the HEC cDNA, followed by
normalization through selective PCR amplification."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEV#1046"
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    organism="Homo sapiens"
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Pred. No. 0.0052;
; Mismatches 0;
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1 (baise 1 to 334)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOllveira, P.S., Bucher, P., Jongeneel, C.V., Brunstein, A., Golveira, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.bb/scripts/gethtml2.pl?tl=RC4&t2=RC4-BN0408-
271100-013-f09&t3=2000-11-27&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                  Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10737800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF752720.1 GI:12079396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF752720 334 bp mRNA linear RC4-BN0408-271100-013-f09 BN0408 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTTATTTTTT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGTTTTATTGTGTTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTTATTTTTT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGTTTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 128
                                                                                                                                                                                                                                              quality sequence start: 29 quality sequence stop: 334. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
/organism="Homo sapiens"
/mol type="mRNN,"
/mol type="mRNN,"
/db_xref="taxon.9606"
/dev_stage="Adult"
/clone lib="BN0408"
/clone lib="BN0408"
/note="Organ: breast normal; Vector: pucl8; Site_1: Smal;
/note_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="invasive ductal carcinoma, 3 pooled samples"
/lab_host="PH108 (T1-phage resistant)"
/clone_lib="NCI_CGAP_Br2"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies."
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/db_xref="taxon:9606"
/clone="IMAGE:3645845"
                                                                                                                                                                                                                             .334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 0.0048;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sao Paulo-SP,
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VERSION KEYWORDS

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                                                               Query Match
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Best Local
                                                                                                                                                                                                                                                                      source
                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 ATTTTATTTTTT 30
                                                                                                                                                                                                                                                                                                                                                                     and -minmacc
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4356
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -min
                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 9 row: L column: 21
Seq primer: ATTTAGGTCACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine gene discovery by normalized cDNA-library sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW347336 337 bp 1
30736 MARC 1PIG Sus scrofa cDNA 5',
AW347336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST cluster assembly Mamm. Genome 13 (8),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW347336.1
                                                 Similarity
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                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                          minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                /clone lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: Library made from pooled tissue from day 11, 13, 1 and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                 /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                 Score 73; DB 10;
Pred. No. 0.0048;
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Pred. No. 0.0048;
                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                               Length 337;
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                                 Indels
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CA771107/c
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138
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1 (bases 1 to 338)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scaece,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Schmitt,A., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

Milliams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Onpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seg primer: -40Up from Gibco
High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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CA771107.1 GI:26008149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
ATTITATTTTTT 126
                                                                                                          AACGTTTTATTGTGTTTTTTAATTTTATTTAGTAGATGGATTCTCAGATATTTTATATTTTTT 139
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                                         ATTTTATTTTTTT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 313.
Location/Qualifiers
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                           /note=Torgan: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: himoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Purified pancreatic islet"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db xref="taxon:9606"
clone="IMAGE:6131937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                             100.0%; Score 73; DB 14; Length 338; 100.0%; Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lib="HR85 islet"
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Best Local
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                                                                         194 AACGITTTATTGTGTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTATATTTTT 135
                    61
                                                                                                                                                                                          73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 339)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA434443

UI-H-DIO-ary-h-05-0-UI.s1 NCI CGAP DIO Homo sapiens cDNA clone
UI-H-DIO-ary-h-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 122-148, ART rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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CA434443.1 GI:24798863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                       Similarity
ATTTTATTTTTTT 73
                                                                                                             AACGTTTAATTGTGTTTTTAATTTAATTTAATGATGGATTCTCAGATATTTTATATTTTT 60
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_DIO"
/clone_lib="NCI_CGAP_DIO"
/clone="Torgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a /notes-"Organ: Lung; Vector: Site 1: Bcor I; Site 2: Not I; modified polylinker; Site 1: Bcor I; Site 2: Not I; NCI_CGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=lung with fibrosis
TAG_LIB=UI-H-DIO
TAG_SEQ=ATACGCGGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="UI-H-DIO-ary-h-05-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                    100.0%; Score 73; DB 14; 100.0%; Pred. No. 0.0047;
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                                                                                                                                                                                             Mismatches
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RESULT 13

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RESULT 14
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AUTHORS
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Best Local :
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JOURNAL
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df27b10.y1 Morton I
IMAGE:2484450 5', n
AW021706
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1 (bases 1 to 350)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB068539 350 bp mRNA linear EST 21-JAN-2003 1829d11.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6553965 3',
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                                                                                                                                                                                                                                                                          AACGTTTTATTGTGTTTTTAATTTTATTTATGAGATGGATTCTCAGATATTTATATTTTT
                                                                                                                                                                      ATTTTATTTTTT 123
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                                                                                                                                                                                                                                                                                                                                                                                                      /lab_nost="white"
/clone_lib="HR85 islet"
/clone_lib="HR85 islet"
/clone_lib="HR85 islet"
/note="lorgan: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="lorgan: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, B-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:6533965"
/tissue_type="Purified pancreatic islet"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
[mol_type="mRNA"]
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                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                     351 bp mRNA linear EST Fetal Cochiea Homo sapiens cDNA clone mRNA sequence.
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Pred. No. 0.0046;
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CB068681/c
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AUTHORS
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                                        Homo sapiens
                                                                                                    CB068681.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                            mRNA sequence.
                                                                                                                                                                                   CB068681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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EST.
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                                                           sapiens
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                                                           (human)
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1 AACGITTTATTGTGTTTTTTAATTTATTTATTAAGATGGATTCTCAGATATTTTATATTTTT 60
                                                                                                                                                        is31d11.x1 HR85 islet Homo sapiens
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Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening genomics 23, 42-50 (1994)
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLAM6182 row: D column: 19
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Brigham and Women's Hospital
75 Francis Street, Harvard Medical School,
Tel: 617 732 7980
Fax: 617 738 6996
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Location/Qualifiers
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Departments of Pathology and Obstetrics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="cochlea"
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/dev stage="16-22 week fetus"
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/note="Organ: ear, Vector: DBluescript SK-, Site_1: EcoRI,
/note="Organ: ear, Vector: DBluescript Stage: S
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/mol_type="mRNA"
/db_xref="taxon:9606"
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GI:27813201
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Pred. No.
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TITLE
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COMMENT
Search completed: October 14, 2004, 18:41:36 Job time : 1922 secs
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 73; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 0.0046; Matches 73; Conservative 0; Mismatches 0; Indels
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                                                                                                                                   137 ATTTTATTTTTT 125
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                                                                                                                                                                         61 ATTTTATTTTTT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrine Pancreas Consortium (Inpublished (2000) (Inpublished (2000) (Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium (Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 352)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J., Kenty, G., Gradwohl, G., Cliffon, S., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Cliffon, S., Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD.
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (clone="IMAGE:6553989"
'tissue_type="Purified pancreatic islet"
'lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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